An investigation of Symbiodiniaceae communities via ITS-2 rDNA amplicon sequencing in Acropora millepora corals from the Great Barrier Reef following exposure to stressors in October 2014

Website: https://www.bco-dmo.org/dataset/844431
Data Type: Other Field Results
Version: 1
Version Date: 2021-03-31

Project
» Collaborative Research: Viral Reefscapes: The Role of Viruses in Coral Reef Health, Disease, and Biogeochemical Cycling (Moorea Virus Project)

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Abstract
Symbiodiniaceae communities were investigated at three locations on the Great Barrier Reef in October 2014. Acropora millepora samples from Davies Reef lagoon (18°30′3.96″S, 147°22′48″E), Rib Reef (18°28′53.4″S, 146°52′24.96″E), and Pandora Island (18°48′45″S, 146°25′59.16″E), were exposed to various stressors including pCO2, heat, bacteria, all of these, or none of these (control). This dataset lists accessions and collection information for ITS-2 rDNA amplicon data that are available at the National Center for Biotechnology Information (NCBI) under BioProject PRJNA596498.

Table of Contents

Coverage

Spatial Extent: **N**:-18.4815 **E**:147.38 **S**:-18.8125 **W**:146.4331
Temporal Extent: 2014-10-01 - 2014-10-08

Methods & Sampling

Symbiodiniaceae communities from Acropora millepora corals were investigated at three locations on the Great Barrier Reef between October 1st and 8th, 2014. Samples from Davies Reef lagoon, Rib Reef, and Pandora Island were collected and snap frozen in liquid nitrogen and stored at -20°C until further processing. DNA was extracted using Wayne's Method (Wilson et al., 2002; Lundgren et al., 2013) from tissue slurry prepared following the method of Wright et al. (2019).

This dataset lists accessions and collection information for ITS-2 rDNA amplicon data from Acropora millepora

corals following exposure to various stressors. Stressors included pCO2, heat, bacteria, all of these, or none of these (control). ITS-2 rDNA Symbiodiniaceae community libraries were prepared and PE 300bp reads were generated using Illumina MiSeq platform. BioSamples and SRA accessions are available at the National Center for Biotechnology Information (NCBI) under BioProject PRJNA596498 (https://www.ncbi.nlm.nih.gov/search/all/?term=PRJNA596498)

Data Processing Description

Demultiplexed fastq files were generated with Illumina's BaseSpaceFS (version 1.5.964) and reads were processed in RStudio (version 1.1.456) through the DADA2 pipeline (version 1.11.0; Callahan et al., 2016) with modifications for the Symbiodiniaceae ITS-2 region. The DADA2 pipeline generated a table of amplicon sequence variants (ASVs). Samples with fewer than 10,000 reads (n = 2) were removed from the dataset.

To identify biologically relevant entities from Symbiodiniaceae ITS-2 sequence data, we applied a post-DADA2 clustering curation using the LULU pipeline (Frøslev et al., 2017). LULU uses co-occurrence patterns and sequence similarity to collapse ITS-2 sequences that likely represent intragenomic variants; we applied thresholds of 95% and 84%, respectively, in this study. Symbiodiniaceae ITS-2 types were then assigned based on BLAST results to a local Symbiodiniaceae ITS-2 database (Cunning et al., 2017).

BCO-DMO processing description:
- Converted latitude and longitude values from DMS to decimal degrees
- Created columns for DD latitude and longitudes for the three sites
- Separated Collection Location into Region and Site
- Added columns for Year and Month of sampling
- Adjusted field/parameter names to comply with database requirements
- Added a conventional header with dataset name, PI names, version date

[table of contents | back to top]

Data Files

File
coral_accessions.csv (Comma Separated Values (.csv), 12.71 KB) MD5:ed7a4a7017903946aee34741f6961907
Primary data file for dataset ID 844431

[table of contents | back to top]

Related Publications

Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). DADA2: High-resolution sample inference from Illumina amplicon data. Nature Methods, 13(7), 581–583. doi:10.1038/nmeth.3869
Methods

Cunning, R., Gates, R. D., & Edmunds, P. J. (2017). Using high-throughput sequencing of ITS2 to describe Symbiodinium metacommunities in St. John, US Virgin Islands. PeerJ, 5, e3472. doi:10.7717/peerj.3472 https://doi.org/https://doi.org/10.7717/peerj.3472
Methods

Frøslev, T. G., Kjøller, R., Bruun, H. H., Ejrnæs, R., Brunbjerg, A. K., Pietroni, C., & Hansen, A. J. (2017).

Algorithm for post-clustering curation of DNA amplicon data yields reliable biodiversity estimates. Nature Communications, 8(1). doi:10.1038/s41467-017-01312-x https://doi.org/https://doi.org/10.1038/s41467-017-01312-x
Methods

Howe-Kerr, L. I., Bachelot, B., Wright, R. M., Kenkel, C. D., Bay, L. K., & Correa, A. M. S. (2020). Symbiont community diversity is more variable in corals that respond poorly to stress. Global Change Biology, 26(4), 2220–2234. doi:10.1111/gcb.14999
Results

Illumina. 16S Metagenomic Sequencing Library Preparation: Preparing 16S Ribosomal RNA Gene Amplicons for the Illumina MiSeq System. (2013). [cited 2018 Oct 18]; Available from: https://support.illumina.com/documents/documentation/chemistry_documentation/16s/16s-metagenomic-library-prep-guide-15044223-b.pdf https://www.illumina.com/content/dam/illumina-support/documents/documentation/chemistry_documentation/16s/16s-metagenomic-library-prep-guide-15044223-b.pdf
Methods

Lundgren, P., Vera, J. C., Peplow, L., Manel, S., & van Oppen, M. J. (2013). Genotype – environment correlations in corals from the Great Barrier Reef. BMC Genetics, 14(1), 9. doi:10.1186/1471-2156-14-9 https://doi.org/https://doi.org/10.1186/1471-2156-14-9
Methods

RStudio Team (2018). RStudio: Integrated Development for R. RStudio, PBC, Boston, MA URL http://www.rstudio.com/.
Software

Wilson, K., Li, Y., Whan, V., Lehnert, S., Byrne, K., Moore, S., Pongsomboon, S., Tassanakajon, A., Rosenberg, G., Ballment, E., Fayazi, Z., Swan, J., Kenway, M., & Benzie, J. (2002). Genetic mapping of the black tiger shrimp Penaeus monodon with amplified fragment length polymorphism. Aquaculture, 204(3–4), 297–309. https://doi.org/10.1016/s0044-8486(01)00842-0 https://doi.org/10.1016/S0044-8486(01)00842-0
Methods

Wright, R.M., Mera, H., Kenkel, C. D., Nayfa, M., Bay, L. K., & Matz, M. V. (2019). Positive genetic associations among fitness traits support evolvability of a reef-building coral under multiple stressors. Global Change Biology, 25(10), 3294–3304. Portico. https://doi.org/10.1111/gcb.14764
Methods

[table of contents | back to top]

Parameters

Parameter	Description	Units
Year	Year of collection	unitless
Month	Month of collection	unitless
Region	Geographical area of sampling	unitless
Site	Site of sampling	unitless
Latitude	Latitude of sampling	decimal degrees
Longitude	Longitude of sampling	decimal degrees
Sample_Name	Sample name	unitless
Genotype_ID	Genotype identifier	unitless
Treatment	Stressor exposure treatment	unitless
Host_Species	Host species	unitless
SRA_Run	NCBI Sequence Read Archive Run identifier	unitless
BioSample_Accession	NCBI BioSample Accession identifier	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina MiSeq platform
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	ITS-2 rDNA Symbiodiniaceae community libraries were prepared and PE 300bp reads were generated using Illumina MiSeq platform
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

[table of contents | back to top]

Project Information

Collaborative Research: Viral Reefscapes: The Role of Viruses in Coral Reef Health, Disease, and Biogeochemical Cycling (Moorea Virus Project)

Coverage: Moorea, French Polynesia, Pacific 17 S 150 W

Ecologically and economically, coral reefs are among the most valuable ecosystems on Earth. These habitats are estimated to harbor up to nine million species, contribute ~30 billion US dollars annually to the global economy, and are tropical epicenters of biogeochemical cycling. Global (climate change) and local (nutrient pollution and overfishing) stressors are drivers of coral reef decline that can disrupt the symbiotic associations among corals and resident microbial communities, including dinoflagellate algae, bacteria, and viruses. Viruses interact with all living cellular organisms, are abundant in oceans, and integral to marine ecosystem functioning. This project will be the first to quantify the variability of viral infection in corals across different reef habitats and across time. This will increase our understanding of the total diversity of coral viruses and illuminate the full suite of factors that trigger viral outbreaks on reefs. At the same time the project will evaluate how carbon and nitrogen cycling are altered on coral reefs as a result of global and local stressors that trigger viral infection. This project will ultimately broaden our understanding of the impacts of viruses on reefs beyond their role as putative disease agents. Results of the project will be communicated broadly in scientific arenas, in K-12, undergraduate, and graduate education and training programs, and to the general public through video and multimedia productions, as well as outreach events. 2-D Reef Replicas from our field sites across Moorea will be constructed, allowing children and adults in the US and French Polynesia to 'become' marine scientists and use quadrats, transect tapes, and identification guides to quantify metrics of reef change. Three graduate students will be involved in all aspects of the research and an effort will be made to recruit and support minority students. All datasets will be made freely available to the public and newly developed methods from this project will serve as an important set of springboard tools and baselines for future lines of inquiry into the processes that influence reef health.

Coral reefs, found in nutrient-poor shallow waters, are biodiversity and productivity hotspots that provide substantial ecological and societal benefits. Corals energetically subsidize these oligotrophic ecosystems by releasing significant amounts of mucus (an organic carbon and nitrogen-rich matrix) into the surrounding seawater. Viral production in reef waters can be a significant portion of total reef carbon cycling, accounting for ~10% of gross benthic carbon fixation in reef ecosystems. Viruses are also ~10 times more abundant on

coral surfaces than in the water column meaning that viral infection experienced by corals during stress likely results is an increase in carbon and perhaps nitrogen flux to the water column. Thus phages and eukaryotic viruses may be responsible for shifting reef health and function directly via coral and symbiont infection and by altering biogeochemical cycling in host colonies and the adjacent reef system. The main goal of this project is to experimentally interrogate and then model the links among viral infections, declines in coral and reef health, and associated shifts in biogeochemical cycling in reef ecosystems. Lab and field experiments will be conducted at the Moorea Coral Reef LTER to characterize the spatiotemporal dynamics of viruses within two dominant reef-building coral species that differ in their susceptibility to abiotic stress. A novel viral infection and induction approach will be coupled with stable isotopic pulse-chase experiments to quantify and track carbon and nitrogen flux out of coral holobionts (host and microbial symbionts) and into dissolved and particulate pools. In these experiments, virus, bacteria, and symbiont abundance, diversity, and function will be measured simultaneously with the health and activity of the host. Pulse-chase techniques, as well as flux- and niche-based modeling, will result in a holistic understanding of how corals and associated viruses impact reef energy budgets and the ramifications of carbon and nitrogen flux for reef communities. Ultimately, this project will quantify and describe an integrated mechanism by which environmental stressors alter viral, microbial, and coral diversity and, consequently, ecosystem function.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1635798

[table of contents | back to top]